



SEQUENCE LISTING

<110> Smith, Michael D.  
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<120> Thermostable Reverse Transcriptases and Uses Thereof

<130> 0942.5040001/RWE/MTT

<140> US 09/845,157

<141> 2001-05-01

<150> US 60/207,196

<151> 2000-05-26

<160> 8

<170> PatentIn version 3.0

<210> 1

<211> 2151

<212> DNA

<213> Moloney-Murine Leukemia Virus

<220>

<221> CDS

<222> (1)..(2151)

<400> 1

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Gly	Gly	Gln	Gln	Met	Gly	Arg	Asp	Leu	Tyr	Asp	Asp	Asp	Asp	Lys	His	
			20					25					30			
atg	acc	cta	aat	ata	gaa	gat	gag	tat	cgg	cta	cat	gag	acc	tca	aaa	144
Met	Thr	Leu	Asn	Ile	Glu	Asp	Glu	Tyr	Arg	Leu	His	Glu	Thr	Ser	Lys	
		35					40					45				
gag	cca	gat	gtt	tct	cta	ggg	tcc	aca	tgg	ctg	tct	gat	ttt	cct	cag	192
Glu	Pro	Asp	Val	Ser	Leu	Gly	Ser	Thr	Trp	Leu	Ser	Asp	Phe	Pro	Gln	
	50					55					60					
gcc	tgg	gcg	gaa	acc	ggg	ggc	atg	gga	ctg	gca	gtt	cgc	caa	gct	cct	240
Ala	Trp	Ala	Glu	Thr	Gly	Gly	Met	Gly	Leu	Ala	Val	Arg	Gln	Ala	Pro	
65					70				75					80		
ctg	atc	ata	ctt	ctg	aaa	gca	acc	tct	acc	ccc	gtg	tcc	ata	aaa	caa	288
Leu	Ile	Ile	Leu	Leu	Lys	Ala	Thr	Ser	Thr	Pro	Val	Ser	Ile	Lys	Gln	
				85					90					95		
tac	ccc	atg	tca	caa	gaa	gcc	aga	ctg	ggg	atc	aag	ccc	cac	ata	cag	336
Tyr	Pro	Met	Ser	Gln	Glu	Ala	Arg	Leu	Gly	Ile	Lys	Pro	His	Ile	Gln	
			100					105					110			
aga	ctg	ttg	gac	cag	gga	ata	ctg	gta	ccc	tgc	cag	tcc	ccc	tgg	aac	384
Arg	Leu	Leu	Asp	Gln	Gly	Ile	Leu	Val	Pro	Cys	Gln	Ser	Pro	Trp	Asn	
		115					120					125				
acg	ccc	ctg	cta	ccc	gtc	aag	aaa	ccc	ggg	act	aat	gat	tac	agg	cct	432
Thr	Pro	Leu	Leu	Pro	Val	Lys	Lys	Pro	Gly	Thr	Asn	Asp	Tyr	Arg	Pro	
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gtc	caa	gat	ctg	aga	gag	gtc	aac	aaa	cgc	gta	gaa	gac	atc	cac	ccc	480
Val	Gln	Asp	Leu	Arg	Glu	Val	Asn	Lys	Arg	Val	Glu	Asp	Ile	His	Pro	
145					150				155						160	
acc	gta	ccc	aac	ccc	tac	aac	ctc	ttg	agt	ggg	ctc	cca	ccg	tcc	cac	528
Thr	Val	Pro	Asn	Pro	Tyr	Asn	Leu	Leu	Ser	Gly	Leu	Pro	Pro	Ser	His	
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cag	tgg	tac	act	gtt	cta	gac	tta	aaa	gat	gcc	ttt	ttc	tgc	ctg	aga	576
Gln	Trp	Tyr	Thr	Val	Leu	Asp	Leu	Lys	Asp	Ala	Phe	Phe	Cys	Leu	Arg	
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ctc	cac	ccg	acg	tct	cag	cct	ctc	ttc	gcc	ttt	gaa	tgg	aga	gac	cca	624
Leu	His	Pro	Thr	Ser	Gln	Pro	Leu	Phe	Ala	Phe	Glu	Trp	Arg	Asp	Pro	
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gag	atg	gga	atc	tct	ggc	caa	cta	acc	tgg	acc	aga	ctc	cca	cag	gga	672
Glu	Met	Gly	Ile	Ser	Gly	Gln	Leu	Thr	Trp	Thr	Arg	Leu	Pro	Gln	Gly	
	210					215					220					
ttc	aaa	aac	agt	ccc	acc	ctg	ttt	gat	gag	gca	ctg	cgc	aga	gac	cta	720
Phe	Lys	Asn	Ser	Pro	Thr	Leu	Phe	Asp	Glu	Ala	Leu	Arg	Arg	Asp	Leu	

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Ala Asp Phe Arg Ile Gln His Pro Asp Leu Ile Leu Leu Gln Tyr Val				
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gat gac tta ctg ctg gcc gcc act tct gag ctc gac tgc caa caa ggt				816
Asp Asp Leu Leu Leu Ala Ala Thr Ser Glu Leu Asp Cys Gln Gln Gly				
	260	265	270	
act cgg gcc ctg tta caa acc cta gga gac ctc ggg tat cgg gcc tcg				864
Thr Arg Ala Leu Leu Gln Thr Leu Gly Asp Leu Gly Tyr Arg Ala Ser				
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gcc aag aaa gcc caa att tgc cag aaa cag gtc aag tat ctg ggg tat				912
Ala Lys Lys Ala Gln Ile Cys Gln Lys Gln Val Lys Tyr Leu Gly Tyr				
	290	295	300	
ctt cta aaa gag ggt cag aga tgg ctg act gag gcc aga aaa gag act				960
Leu Leu Lys Glu Gly Gln Arg Trp Leu Thr Glu Ala Arg Lys Glu Thr				
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gtg atg ggg cag cct act ccg aag acc ccg cgg caa cta agg gag ttc				1008
Val Met Gly Gln Pro Thr Pro Lys Thr Pro Arg Gln Leu Arg Glu Phe				
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cta ggg acg gca ggc ttc tgt cgc ctc tgg atc cct ggg ttt gca gaa				1056
Leu Gly Thr Ala Gly Phe Cys Arg Leu Trp Ile Pro Gly Phe Ala Glu				
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tgg ggc cca gac caa caa aag gcc tat caa gaa atc aag caa gct ctt				1152
Trp Gly Pro Asp Gln Gln Lys Ala Tyr Gln Glu Ile Lys Gln Ala Leu				
	370	375	380	
cta act gcc cca gcc ctg ggg ttg cca gat ttg act aag ccc ttt gaa				1200
Leu Thr Ala Pro Ala Leu Gly Leu Pro Asp Leu Thr Lys Pro Phe Glu				
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ctc ttt gtc gac gag aag cag ggc tac gcc aaa ggt gtc cta acg caa				1248
Leu Phe Val Asp Glu Lys Gln Gly Tyr Ala Lys Gly Val Leu Thr Gln				
	405	410	415	
aaa ctg gga cct tgg cgt cgg ccg gtg gcc tac ctg tcc aaa aag cta				1296
Lys Leu Gly Pro Trp Arg Arg Pro Val Ala Tyr Leu Ser Lys Lys Leu				
	420	425	430	
gac cca gta gca gct ggg tgg ccc cct tgc cta cgg atg gta gca gcc				1344
Asp Pro Val Ala Ala Gly Trp Pro Pro Cys Leu Arg Met Val Ala Ala				
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att gcc gta ctg aca aag gat gca ggc aag cta acc atg gga cag cca				1392
Ile Ala Val Leu Thr Lys Asp Ala Gly Lys Leu Thr Met Gly Gln Pro				
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cta gtc att ctg gcc ccc cat gca gta gag gca cta gtc aaa caa ccc Leu Val Ile Leu Ala Pro His Ala Val Glu Ala Leu Val Lys Gln Pro 465 470 475 480	1440
ccc gat cga tgg ctt tcc aac gcc cgg atg act cac tat cag gcc ttg Pro Asp Arg Trp Leu Ser Asn Ala Arg Met Thr His Tyr Gln Ala Leu 485 490 495	1488
ctt ttg gac acg gac cgg gtc cag ttc gga ccg gtg gta gcc ctg aac Leu Leu Asp Thr Asp Arg Val Gln Phe Gly Pro Val Val Ala Leu Asn 500 505 510	1536
ccg gct aca ctg ctc cca ctg cct gag gaa ggg ctg cag cac aac tgc Pro Ala Thr Leu Leu Pro Leu Pro Glu Glu Gly Leu Gln His Asn Cys 515 520 525	1584
ctt gat atc ctg gcc gaa gcc cac gga acc cga ccc gac cta acg gac Leu Asp Ile Leu Ala Glu Ala His Gly Thr Arg Pro Asp Leu Thr Asp 530 535 540	1632
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ctc ttg caa gag gga cag cgt aag gcg gga gct gcg gtg acc acc gag Leu Leu Gln Glu Gly Gln Arg Lys Ala Gly Ala Ala Val Thr Thr Glu 565 570 575	1728
acc gag gta atc tgg gct aaa gcc ctg cca gcc ggg aca tcc gct cag Thr Glu Val Ile Trp Ala Lys Ala Leu Pro Ala Gly Thr Ser Ala Gln 580 585 590	1776
cgg gct cag ctg ata gca ctc acc cag gcc cta agg atg gca gaa ggt Arg Ala Gln Leu Ile Ala Leu Thr Gln Ala Leu Arg Met Ala Glu Gly 595 600 605	1824
aag aag cta aat gtt tat acg aat tcc cgt tat gct ttt gct act gcc Lys Lys Leu Asn Val Tyr Asn Ser Arg Tyr Ala Phe Ala Thr Ala 610 615 620	1872
cat atc cat gga gaa ata tac aga agg cgt ggg ttg ctc aca tca gaa His Ile His Gly Glu Ile Tyr Arg Arg Gly Leu Leu Thr Ser Glu 625 630 635 640	1920
ggc aaa gag atc aaa aat aag gac gag ata ttg gcc cta cta aaa gcc Gly Lys Glu Ile Lys Asn Lys Asp Glu Ile Leu Ala Leu Leu Lys Ala 645 650 655	1968
ctc ttt ctg ccc aaa aga ctt agc ata atc cat tgt cca gga cat caa Leu Phe Leu Pro Lys Arg Leu Ser Ile Ile His Cys Pro Gly His Gln 660 665 670	2016
aag gga cac agc gcc gag gct aga ggc aac cgg atg gct gac caa gcg Lys Gly His Ser Ala Glu Ala Arg Gly Asn Arg Met Ala Asp Gln Ala 675 680 685	2064

gcc cga aag gca gcc atc aca gag aat cca gac acc tct acc ctc ctc 2112  
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 690 695 700

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<212> PRT

<213> Moloney-Murine Leukemia Virus

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Met Gly Gly Ser His His His His His His Gly Met Ala Ser Met Thr  
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 20 25 30

Met Thr Leu Asn Ile Glu Asp Glu Tyr Arg Leu His Glu Thr Ser Lys  
 35 40 45

Glu Pro Asp Val Ser Leu Gly Ser Thr Trp Leu Ser Asp Phe Pro Gln  
 50 55 60

Ala Trp Ala Glu Thr Gly Gly Met Gly Leu Ala Val Arg Gln Ala Pro  
 65 70 75 80

Leu Ile Ile Leu Leu Lys Ala Thr Ser Thr Pro Val Ser Ile Lys Gln  
 85 90 95

Tyr Pro Met Ser Gln Glu Ala Arg Leu Gly Ile Lys Pro His Ile Gln  
 100 105 110

Arg Leu Leu Asp Gln Gly Ile Leu Val Pro Cys Gln Ser Pro Trp Asn  
 115 120 125

Thr Pro Leu Leu Pro Val Lys Lys Pro Gly Thr Asn Asp Tyr Arg Pro  
 130 135 140

Val Gln Asp Leu Arg Glu Val Asn Lys Arg Val Glu Asp Ile His Pro

145		150		155		160
Thr Val Pro Asn	Pro Tyr Asn Leu Leu Ser Gly Leu Pro Pro Ser His					
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Gln Trp Tyr Thr Val Leu Asp Leu Lys Asp Ala Phe Phe Cys Leu Arg						
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Leu His Pro Thr Ser Gln Pro Leu Phe Ala Phe Glu Trp Arg Asp Pro						
	195		200			205
Glu Met Gly Ile Ser Gly Gln Leu Thr Trp Thr Arg Leu Pro Gln Gly						
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Phe Lys Asn Ser Pro Thr Leu Phe Asp Glu Ala Leu Arg Arg Asp Leu						
	225		230		235	240
Ala Asp Phe Arg Ile Gln His Pro Asp Leu Ile Leu Leu Gln Tyr Val						
		245		250		255
Asp Asp Leu Leu Leu Ala Ala Thr Ser Glu Leu Asp Cys Gln Gln Gly						
		260		265		270
Thr Arg Ala Leu Leu Gln Thr Leu Gly Asp Leu Gly Tyr Arg Ala Ser						
	275		280			285
Ala Lys Lys Ala Gln Ile Cys Gln Lys Gln Val Lys Tyr Leu Gly Tyr						
	290		295			300
Leu Leu Lys Glu Gly Gln Arg Trp Leu Thr Glu Ala Arg Lys Glu Thr						
	305		310		315	320
Val Met Gly Gln Pro Thr Pro Lys Thr Pro Arg Gln Leu Arg Glu Phe						
		325		330		335
Leu Gly Thr Ala Gly Phe Cys Arg Leu Trp Ile Pro Gly Phe Ala Glu						
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Met Ala Ala Pro Leu Tyr Pro Leu Thr Lys Thr Gly Thr Leu Phe Asn						
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Trp Gly Pro Asp Gln Gln Lys Ala Tyr Gln Glu Ile Lys Gln Ala Leu						
	370		375			380

Leu Thr Ala Pro Ala Leu Gly Leu Pro Asp Leu Thr Lys Pro Phe Glu  
385 390 395 400

Leu Phe Val Asp Glu Lys Gln Gly Tyr Ala Lys Gly Val Leu Thr Gln  
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Lys Leu Gly Pro Trp Arg Arg Pro Val Ala Tyr Leu Ser Lys Lys Leu  
420 425 430

Asp Pro Val Ala Ala Gly Trp Pro Pro Cys Leu Arg Met Val Ala Ala  
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Ile Ala Val Leu Thr Lys Asp Ala Gly Lys Leu Thr Met Gly Gln Pro  
450 455 460

Leu Val Ile Leu Ala Pro His Ala Val Glu Ala Leu Val Lys Gln Pro  
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Pro Asp Arg Trp Leu Ser Asn Ala Arg Met Thr His Tyr Gln Ala Leu  
485 490 495

Leu Leu Asp Thr Asp Arg Val Gln Phe Gly Pro Val Val Ala Leu Asn  
500 505 510

Pro Ala Thr Leu Leu Pro Leu Pro Glu Glu Gly Leu Gln His Asn Cys  
515 520 525

Leu Asp Ile Leu Ala Glu Ala His Gly Thr Arg Pro Asp Leu Thr Asp  
530 535 540

Gln Pro Leu Pro Asp Ala Asp His Thr Trp Tyr Thr Gly Gly Ser Ser  
545 550 555 560

Leu Leu Gln Glu Gly Gln Arg Lys Ala Gly Ala Ala Val Thr Thr Glu  
565 570 575

Thr Glu Val Ile Trp Ala Lys Ala Leu Pro Ala Gly Thr Ser Ala Gln  
580 585 590

Arg Ala Gln Leu Ile Ala Leu Thr Gln Ala Leu Arg Met Ala Glu Gly  
595 600 605

Lys Lys Leu Asn Val Tyr Thr Asn Ser Arg Tyr Ala Phe Ala Thr Ala  
610 615 620

His Ile His Gly Glu Ile Tyr Arg Arg Arg Gly Leu Leu Thr Ser Glu  
625 630 635 640

Gly Lys Glu Ile Lys Asn Lys Asp Glu Ile Leu Ala Leu Leu Lys Ala  
645 650 655

Leu Phe Leu Pro Lys Arg Leu Ser Ile Ile His Cys Pro Gly His Gln  
660 665 670

Lys Gly His Ser Ala Glu Ala Arg Gly Asn Arg Met Ala Asp Gln Ala  
675 680 685

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Ile Glu Asn Ser Ser Pro Asn Ser Arg Leu Ile Asn  
705 710 715

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<211> 47

<212> DNA

<213> Artificial

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<223> Oligonucleotide template

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<210> 4

<211> 18

<212> DNA

<213> Artificial

<220>



<223> Oligonucleotide primer

<400> 4

cttccattca cacactgc

18

<210> 5

<211> 21

<212> DNA

<213> Artificial

<220>

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<400> 5

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21

<210> 6

<211> 298

<212> DNA

<213> Escherichia coli

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gctatgacca tgattacgcc aagcttgcac gcctgcaggt cgactctaga ggatccccgg 180

gtaccgagct cgaattcact ggccgctcgtt ttacaacgct gtgactggga aaaccctggc 240

gttaccacac ttaatcgctt tgcagcacat ccccttttcg ccagctggcg taatagcg 298

<210> 7

<211> 1575

<212> DNA

<213> Moloney-Murine Leukemia Virus

<220>

<221> CDS

<222> (1)..(1575)

<400> 7

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Glu Pro Asp Val Ser Leu Gly Ser Thr Trp Leu Ser Asp Phe Pro Gln	
20 25 30	
 gcc tgg gcg gaa acc ggg ggc atg gga ctg gca gtt cgc caa gct cct	144
Ala Trp Ala Glu Thr Gly Gly Met Gly Leu Ala Val Arg Gln Ala Pro	
35 40 45	
 ctg atc ata cct ctg aaa gca acc tct acc ccc gtg tcc ata aaa caa	192
Leu Ile Ile Pro Leu Lys Ala Thr Ser Thr Pro Val Ser Ile Lys Gln	
50 55 60	
 tac ccc atg tca caa gaa gcc aga ctg ggg atc aag ccc cac ata cag	240
Tyr Pro Met Ser Gln Glu Ala Arg Leu Gly Ile Lys Pro His Ile Gln	
65 70 75 80	
 aga ctg ttg gac cag gga ata ctg gta ccc tgc cag tcc ccc tgg aac	288
Arg Leu Leu Asp Gln Gly Ile Leu Val Pro Cys Gln Ser Pro Trp Asn	
85 90 95	
 acg ccc ctg cta ccc gtt aag aaa cca ggg act aat gat tat agg cct	336
Thr Pro Leu Leu Pro Val Lys Lys Pro Gly Thr Asn Asp Tyr Arg Pro	
100 105 110	
 gtc cag gat ctg aga gaa gtc aac aag cgg gtg gaa gac atc cac ccc	384
Val Gln Asp Leu Arg Glu Val Asn Lys Arg Val Glu Asp Ile His Pro	
115 120 125	
 acc gtg ccc aac cct tac aac ctc ttg agc ggg ctc aag cgg gtg gaa	432
Thr Val Pro Asn Pro Tyr Asn Leu Leu Ser Gly Leu Lys Arg Val Glu	
130 135 140	
 gac atc cac ccc acc gtg ccc aac cct tac aac ctc ttg agc ggg ctc	480
Asp Ile His Pro Thr Val Pro Asn Pro Tyr Asn Leu Leu Ser Gly Leu	
145 150 155 160	
 cca ccg tcc cac cag tgg tac act gtg ctt gat tta aag gat gcc ttt	528
Pro Pro Ser His Gln Trp Tyr Thr Val Leu Asp Leu Lys Asp Ala Phe	
165 170 175	
 ttc tgc ctg aga ctc cac ccc acc agt cag cct ctc ttc gcc ttt gag	576
Phe Cys Leu Arg Leu His Pro Thr Ser Gln Pro Leu Phe Ala Phe Glu	
180 185 190	

tgg aga gat cca gag atg gga atc tca gga caa ttg acc tgg acc aga	624
Trp Arg Asp Pro Glu Met Gly Ile Ser Gly Gln Leu Thr Trp Thr Arg	
195 200 205	
ctc cca cag ggt ttc aaa aac agt ccc acc ctg ttt gat gag gca ctg	672
Leu Pro Gln Gly Phe Lys Asn Ser Pro Thr Leu Phe Asp Glu Ala Leu	
210 215 220	
cac aga gac cta gca gac ttc cgg atc cag cac cca gac ttg atc ctg	720
His Arg Asp Leu Ala Asp Phe Arg Ile Gln His Pro Asp Leu Ile Leu	
225 230 235 240	
cta cag tac gtg gat gac tta ctg ctg gcc gcc act tct gag cta gac	768
Leu Gln Tyr Val Asp Asp Leu Leu Leu Ala Ala Thr Ser Glu Leu Asp	
245 250 255	
tgc caa caa ggt act cgg gcc ctg tta caa acc cta ggg aac ctc ggg	816
Cys Gln Gln Gly Thr Arg Ala Leu Leu Gln Thr Leu Gly Asn Leu Gly	
260 265 270	
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Tyr Arg Ala Ser Ala Lys Lys Ala Gln Ile Cys Gln Lys Gln Val Lys	
275 280 285	
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Tyr Leu Gly Tyr Leu Leu Lys Glu Gly Gln Arg Trp Leu Thr Glu Ala	
290 295 300	
aga aaa gag act gtg atg ggg cag cct act ccg aag acc cct cga caa	960
Arg Lys Glu Thr Val Met Gly Gln Pro Thr Pro Lys Thr Pro Arg Gln	
305 310 315 320	
cta agg gag ttc cta ggg acg gca ggc ttc tgt cgc ctc tgg atc cct	1008
Leu Arg Glu Phe Leu Gly Thr Ala Gly Phe Cys Arg Leu Trp Ile Pro	
325 330 335	
ggg ttt gca gaa atg gca gcc ccc ttg tac cct ctc acc aaa acg ggg	1056
Gly Phe Ala Glu Met Ala Ala Pro Leu Tyr Pro Leu Thr Lys Thr Gly	
340 345 350	
act ctg ttt aat tgg ggc cca gac caa caa aag gcc tat caa gaa atc	1104
Thr Leu Phe Asn Trp Gly Pro Asp Gln Gln Lys Ala Tyr Gln Glu Ile	
355 360 365	
aag caa gct ctt cta act gcc cca gcc ctg ggg ttg cca gat ttg act	1152
Lys Gln Ala Leu Leu Thr Ala Pro Ala Leu Gly Leu Pro Asp Leu Thr	
370 375 380	
aag ccc ttt gaa ctc ttt gtc gac gag aag cag ggc tac gcc aaa ggt	1200
Lys Pro Phe Glu Leu Phe Val Asp Glu Lys Gln Gly Tyr Ala Lys Gly	
385 390 395 400	
gtc cta acg caa aaa ctg gga cct tgg cgt cgg ccg gtg gcc tac ctg	1248
Val Leu Thr Gln Lys Leu Gly Pro Trp Arg Arg Pro Val Ala Tyr Leu	
405 410 415	
tcc aaa aag cta gac cca gta gca gct ggg tgg ccc cct tgc cta cgg	1296

Ser	Lys	Lys	Leu	Asp	Pro	Val	Ala	Ala	Gly	Trp	Pro	Pro	Cys	Leu	Arg	
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Met	Val	Ala	Ala	Ile	Ala	Val	Leu	Thr	Lys	Asp	Ala	Gly	Lys	Leu	Thr	
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atg	gga	cag	cca	cta	gtc	att	ctg	gcc	ccc	cat	gca	gta	gag	gca	cta	1392
Met	Gly	Gln	Pro	Leu	Val	Ile	Leu	Ala	Pro	His	Ala	Val	Glu	Ala	Leu	
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Val	Lys	Gln	Pro	Pro	Asp	Arg	Trp	Leu	Ser	Asn	Ala	Arg	Met	Thr	His	
465					470				475						480	
tat	cag	gcc	ttg	ctt	ttg	gac	acg	gac	cgg	gtc	cag	ttc	gga	ccg	gtg	1488
Tyr	Gln	Ala	Leu	Leu	Leu	Asp	Thr	Asp	Arg	Val	Gln	Phe	Gly	Pro	Val	
			485					490					495			
gta	gcc	ctg	aac	ccg	gct	acg	ctg	ctc	cca	ctg	cct	gag	gaa	ggg	ctg	1536
Val	Ala	Leu	Asn	Pro	Ala	Thr	Leu	Leu	Pro	Leu	Pro	Glu	Glu	Gly	Leu	
		500					505					510				
caa	cac	aac	tgc	ctt	gat	aat	tcc	cgc	tta	att	aat	taa				1575
Gln	His	Asn	Cys	Leu	Asp	Asn	Ser	Arg	Leu	Ile	Asn					
		515				520										

<210> 8

<211> 524

<212> PRT

<213> Moloney-Murine Leukemia Virus

<400> 8

Met	Thr	Leu	Asn	Ile	Glu	Asp	Glu	His	Arg	Leu	His	Glu	Thr	Ser	Lys
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Glu	Pro	Asp	Val	Ser	Leu	Gly	Ser	Thr	Trp	Leu	Ser	Asp	Phe	Pro	Gln
		20					25						30		

Ala	Trp	Ala	Glu	Thr	Gly	Gly	Met	Gly	Leu	Ala	Val	Arg	Gln	Ala	Pro
	35						40					45			

Leu	Ile	Ile	Pro	Leu	Lys	Ala	Thr	Ser	Thr	Pro	Val	Ser	Ile	Lys	Gln
	50					55				60					

Tyr	Pro	Met	Ser	Gln	Glu	Ala	Arg	Leu	Gly	Ile	Lys	Pro	His	Ile	Gln
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

65		70		75		80									
Arg	Leu	Leu	Asp	Gln	Gly	Ile	Leu	Val	Pro	Cys	Gln	Ser	Pro	Trp	Asn
			85						90					95	
Thr	Pro	Leu	Leu	Pro	Val	Lys	Lys	Pro	Gly	Thr	Asn	Asp	Tyr	Arg	Pro
		100						105					110		
Val	Gln	Asp	Leu	Arg	Glu	Val	Asn	Lys	Arg	Val	Glu	Asp	Ile	His	Pro
		115					120					125			
Thr	Val	Pro	Asn	Pro	Tyr	Asn	Leu	Leu	Ser	Gly	Leu	Lys	Arg	Val	Glu
	130					135					140				
Asp	Ile	His	Pro	Thr	Val	Pro	Asn	Pro	Tyr	Asn	Leu	Leu	Ser	Gly	Leu
145					150					155					160
Pro	Pro	Ser	His	Gln	Trp	Tyr	Thr	Val	Leu	Asp	Leu	Lys	Asp	Ala	Phe
			165						170					175	
Phe	Cys	Leu	Arg	Leu	His	Pro	Thr	Ser	Gln	Pro	Leu	Phe	Ala	Phe	Glu
		180						185					190		
Trp	Arg	Asp	Pro	Glu	Met	Gly	Ile	Ser	Gly	Gln	Leu	Thr	Trp	Thr	Arg
	195						200					205			
Leu	Pro	Gln	Gly	Phe	Lys	Asn	Ser	Pro	Thr	Leu	Phe	Asp	Glu	Ala	Leu
	210					215					220				
His	Arg	Asp	Leu	Ala	Asp	Phe	Arg	Ile	Gln	His	Pro	Asp	Leu	Ile	Leu
225					230					235					240
Leu	Gln	Tyr	Val	Asp	Asp	Leu	Leu	Leu	Ala	Ala	Thr	Ser	Glu	Leu	Asp
			245						250					255	
Cys	Gln	Gln	Gly	Thr	Arg	Ala	Leu	Leu	Gln	Thr	Leu	Gly	Asn	Leu	Gly
			260					265					270		
Tyr	Arg	Ala	Ser	Ala	Lys	Lys	Ala	Gln	Ile	Cys	Gln	Lys	Gln	Val	Lys
	275						280					285			
Tyr	Leu	Gly	Tyr	Leu	Leu	Lys	Glu	Gly	Gln	Arg	Trp	Leu	Thr	Glu	Ala
	290					295					300				

Arg Lys Glu Thr Val Met Gly Gln Pro Thr Pro Lys Thr Pro Arg Gln  
305 310 315 320

Leu Arg Glu Phe Leu Gly Thr Ala Gly Phe Cys Arg Leu Trp Ile Pro  
325 330 335

Gly Phe Ala Glu Met Ala Ala Pro Leu Tyr Pro Leu Thr Lys Thr Gly  
340 345 350

Thr Leu Phe Asn Trp Gly Pro Asp Gln Gln Lys Ala Tyr Gln Glu Ile  
355 360 365

Lys Gln Ala Leu Leu Thr Ala Pro Ala Leu Gly Leu Pro Asp Leu Thr  
370 375 380

Lys Pro Phe Glu Leu Phe Val Asp Glu Lys Gln Gly Tyr Ala Lys Gly  
385 390 395 400

Val Leu Thr Gln Lys Leu Gly Pro Trp Arg Arg Pro Val Ala Tyr Leu  
405 410 415

Ser Lys Lys Leu Asp Pro Val Ala Ala Gly Trp Pro Pro Cys Leu Arg  
420 425 430

Met Val Ala Ala Ile Ala Val Leu Thr Lys Asp Ala Gly Lys Leu Thr  
435 440 445

Met Gly Gln Pro Leu Val Ile Leu Ala Pro His Ala Val Glu Ala Leu  
450 455 460

Val Lys Gln Pro Pro Asp Arg Trp Leu Ser Asn Ala Arg Met Thr His  
465 470 475 480

Tyr Gln Ala Leu Leu Leu Asp Thr Asp Arg Val Gln Phe Gly Pro Val  
485 490 495

Val Ala Leu Asn Pro Ala Thr Leu Leu Pro Leu Pro Glu Glu Gly Leu  
500 505 510

Gln His Asn Cys Leu Asp Asn Ser Arg Leu Ile Asn  
515 520



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re application of:

Michael D. SMITH *et al.*

Appl. No.: 09/845,157

Filed: May 1, 2001

For: **Thermostable Reverse Transcriptases  
and Uses Thereof**

Confirmation No.: 2674

Art Unit: 1637

Examiner: Fredman, Jeffrey N.

Atty. Docket: 0942.5040001/RWE/HCC

**Amendment and Submission of Substitute Sequence Listing  
Under 37 C.F.R. § 1.825(a)**

Commissioner for Patents  
PO Box 1450  
Alexandria, VA 22313-1450

Sir:

In compliance with 37 C.F.R. § 1.825(a), Applicants submit substitute sheets to amend the paper copy of the Sequence Listing.

***In the Specification:***

Please cancel the existing Sequence Listing for the above-identified application, replace it with the substitute Sequence Listing appended hereto, and insert the same at the end of the application.

***Remarks***

The changes made in the sequence listing do not include new matter. Support for these amendments can be found in the specification as originally filed on page 34, paragraph 0092, wherein U.S. Patent No. 5,668,005 is incorporated by reference. The specification has been amended to direct the entry of this corrected Sequence Listing at the end of the above identified application.

In accordance with 37 C.F.R. § 1.825(a), this submission contains no new matter.

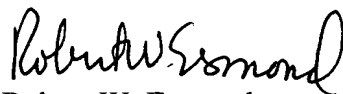
In accordance with 37 C.F.R. § 1.825(b), the paper copy of the Sequence Listing and the computer readable copy of the Sequence Listing submitted herewith are the same.

***Summary***

It is respectfully believed this application is now in condition for allowance. Early notice to this effect is earnestly solicited.

Respectfully submitted,

STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.



Robert W. Esmond  
Attorney for Applicants  
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Date: October 12, 2004

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